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RAW SEQUENCE LISTING                    DATE: 02/26/2002
PATENT APPLICATION:  US/09/941,945A     TIME: 09:39:17

        Input Set : A:\032301.190.seq.ST25.txt
        Output Set: N:\CRF3\02262002\I941945A.raw


   3  <110> APPLICANT: BATHE, Brigitte, et al.
   5  <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE sigD GENE
   7  <130> FILE REFERENCE: 032301 WD 190
C-->  9  <140> CURRENT APPLICATION NUMBER: US/09/941,945A
C-->  9  <141> CURRENT FILING DATE: 2001-08-30
   9  <160> NUMBER OF SEQ ID NOS: 2
  11  <170> SOFTWARE: PatentIn version 3.1
  13  <210> SEQ ID NO: 1
  14  <211> LENGTH: 1129
  15  <212> TYPE: DNA
  16  <213> ORGANISM: Corynebacterium glutamicum
  18  <220> FEATURE:
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  20  <222> LOCATION: (301)..(864)
  21  <223> OTHER INFORMATION:
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  29  tgggtgttat ctgtcagtat gtgaggagat caaggtgttg ggggttctag ttgctaagat   180
  31  ggtgaaaacc cgtgaggcca aaatccaact gggtgaatta cccctgcata aatgcatgag   240
  33  ggctttatac ttgtcttatt attaaacttt tagggttttg atgcaggaag gtgcgagaac   300
  35  ttg gct gat act gag cgc gag ctc gct gac ctg gta ccg cag gca acg   348
  36  Met Ala Asp Thr Glu Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr
  37  1               5                   10                  15
  39  gcg ggc gat cgt cgg gca ttg caa aga ata atg gag att att cac ccc   396
  40  Ala Gly Asp Arg Arg Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro
  41              20                  25                  30
  43  att gtt ttg cgt tat gct cgc gct cgt att gga ggt gga cgc cag cca   444
  44  Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro
  45          35                  40                  45
  47  acg gca gaa gac gtt gct caa gaa atc tgc ctg gcg gta gcc acc tcc   492
  48  Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser
  49      50                  55                  60
  51  att agg aac ttt gtc gac cag ggt agg ccg ttc atg gcg ttt gtc tac   540
  52  Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr
  53  65                  70                  75                  80
  55  ggc att gca tct aac aag gtc gca gat gct cac agg gcg atg tcg agg   588
  56  Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg
  57                  85                  90                  95
  59  gat aaa tcg act cct att gag gaa gtc cca gaa act tca cca gat act   636
  60  Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr
  61                  100                 105                 110
  63  ttt acc ccc gaa gac ttt gcg ctg gtc agc gat gga agt aac aga gtt   684
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64 Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val
65         115             120             125
67 agg gaa ctt ctc gat cta ctg agt gaa aag gca cgc gac att ctt atc         732
68 Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile
69         130             135             140
71 ttg aga gtt atc gtt ggt ctt tcc gca gaa gaa act gca gag atg gtg         780
72 Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val
73 145             150             155             160
75 ggc agc acc cca ggt gct gta cga gtt gcc caa cac agg gca ctc acg         828
76 Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr
77             165             170             175
79 aca ctt cga agc aca ctt gag cag cag gag aac aag taatgactcg            874
80 Thr Leu Arg Ser Thr Leu Glu Gln Gln Glu Asn Lys
81         180             185
83 acgtctacat ggtggtgagc aggatggcca ggaacacgtt aaaggacagc taaagcagct         934
85 gttcgacgac gacgcgttct tgactgacct gtcccgcggc gttgatccct cagagggcga         994
87 tgacgccctc gctggcctcc tcctcgattt aacaaaggaa gctcaggagc cgccggcaac        1054
89 aatgccggat tggtctactt tgctccctgg aattttggat caggatcagg atttgccagt        1114
91 ggaatccact tcgga                                                          1129
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95 <211> LENGTH: 188
96 <212> TYPE: PRT
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106             20              25              30
109 Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro
110             35              40              45
113 Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser
114     50              55              60
117 Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr
118 65              70              75              80
121 Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg
122             85              90              95
125 Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr
126             100             105             110
129 Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val
130         115             120             125
133 Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile
134     130             135             140
137 Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val
138 145             150             155             160
141 Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr
142             165             170             175
145 Thr Leu Arg Ser Thr Leu Glu Gln Gln Glu Asn Lys
146         180             185
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VERIFICATION SUMMARY   DATE: 02/26/2002
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date